RAW SEQUENCE LISTING DATE: 01/02/2001
PATENT APPLICATION: US/09/733,685 TIME: 12:08:29

Input Set : A:\PTO.txt
Output Set: N:\CRF3\01022001\I733685.raw

P5

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      3 <110> APPLICANT: Cade, Rebecca M
      4       Dietrich, Robert A
      6 <120> TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
      7       SAR GENE EXPRESSION IN PLANTS
      9 <130> FILE REFERENCE: A-31089A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/733,685
C--> 12 <141> CURRENT FILING DATE: 2000-12-08
     14 <150> PRIOR APPLICATION NUMBER: 60/171,008
     15 <151> PRIOR FILING DATE: 1999-12-15
     17 <150> PRIOR APPLICATION NUMBER: 60/175,519
     18 <151> PRIOR FILING DATE: 2000-01-11
     20 <160> NUMBER OF SEQ ID NOS: 23
     22 <170> SOFTWARE: PatentIn Ver. 2.1
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 509
     26 <212> TYPE: DNA
     27 <213> ORGANISM: Arabidopsis thaliana
     29 <220> FEATURE:
     30 <221> NAME/KEY: CDS
     31 <222> LOCATION: (68)..(433)
     32 <223> OTHER INFORMATION: gene product NI16
     34 <220> FEATURE:
     35 <221> NAME/KEY: misc_feature
     36 <222> LOCATION: (142)..(147)
     37 <223> OTHER INFORMATION: SalI site
     39 <220> FEATURE:
     40 <221> NAME/KEY: misc_feature
     41 <222> LOCATION: (344)..(349)
     42 <223> OTHER INFORMATION: EcoRI site
     44 <400> SEQUENCE: 1
     45 aaaatcagca aataaacttt tcttgactaa gcttaaacga cgccgttaac attttcttct 60
     47 ggctaac atg aac aac tct ttg aag aaa gaa gaa cgc gta gaa gaa gat   109
     48         Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp
     49           1               5                  10
     51 aac gga aaa tct gac ggt aac aga ggg aaa ccg tcg acg gaa gtt gtt   157
     52 Asn Gly Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val
     53  15                  20                  25                  30
     55 cgg acg gta acg gag gaa gag gtg gat gag ttt ttc aag ata tta cgg   205
     56 Arg Thr Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg
     57                  35                  40                  45
     59 aga gta cac gtg gcg aca cga acg gtt gcg aaa gtt aac ggc ggt gtt   253
     60 Arg Val His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val
     61              50                  55                  60
     63 gct gag gga gag tta ccg tct aag aag agg aaa cgg agt cag aat ctt   301
     64 Ala Glu Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu
     65          65                  70                  75
     67 ggg ttg aga aac tcg ttg gat tgt aac ggc gtt cga gac gga gaa ttc   349
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68 Gly Leu Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe
69      80                  85                  90
71 gat gag att aat cgg gtc ggg tta cag ggt ttg ggt ttg gat ctg aac   397
72 Asp Glu Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn
73  95                 100                 105                 110
75 tgt aaa ccg gaa cca gac agc gtt agt tta tcg ttg tagacttgta       443
76 Cys Lys Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
77                 115                 120
79 gtccttcatg ttttcccccr tcttacaata atcaattttt ttttaactac aatacttttg 503
81 aaaaaa                                                          509
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 122
86 <212> TYPE: PRT
87 <213> ORGANISM: Arabidopsis thaliana
89 <400> SEQUENCE: 2
90 Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp Asn Gly
91   1               5                  10                  15
93 Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val Arg Thr
94              20                  25                  30
96 Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg Arg Val
97          35                  40                  45
99 His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val Ala Glu
100     50                  55                  60
102 Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu Gly Leu
103 65                  70                  75                  80
105 Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe Asp Glu
106                 85                  90                  95
108 Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn Cys Lys
109             100                 105                 110
111 Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
112         115                 120
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1700
118 <212> TYPE: DNA
119 <213> ORGANISM: Arabidopsis thaliana
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (365)..(371)
124 <223> OTHER INFORMATION: TCA1 motif
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (426)..(435)
129 <223> OTHER INFORMATION: TCA1 motif
131 <220> FEATURE:
132 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (609)..(614)
134 <223> OTHER INFORMATION: MYCATR22 element
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature
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138 <222> LOCATION: (646)..(665)
139 <223> OTHER INFORMATION: CAMV AS1 salicylic acid response element
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (707)..(712)
144 <223> OTHER INFORMATION: PAL BOX
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (757)..(762)
149 <223> OTHER INFORMATION: HEXAMERAT 4 element
151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: (863)..(1228)
154 <223> OTHER INFORMATION: NT16 genomic coding region
156 <400> SEQUENCE: 3
157 tgggttttta ttggataaca tgacaaatat ttatttattt catgagtttt tattggatag 60
158 catgacaaat attaatatat cagtgttaat aacatgtttt gttcttaaaa tacatgcatt 120
159 ttaaaatcag acatttgttt taaaatcaaa tctaatctct tatatcacaa cgacattgac 180
160 ggaaaattca ggtaaaaaga gaaaataaag aatgagagat agagagattt ctatggaaaa 240
161 agaaagagag aacatgtagg tgaacaaaat aaagagatat gatgatatat tttatgagag 300
162 gtggtgaaga ttattttagg agagggagag agaaatagaa aaagaaaatg acatggtgaa 360
163 tctgaagaag atgaattgtg ttaaagatga agagagaaag agaactccat ggctaaagtc 420
164 tcgtaaagaa gatgaaaaag aaacaaaaga aggaagaaga aagagaaagg ctaaaataga 480
165 ctaactattg ccaaaatttc tgtagccgac aaatactatt tggtccaagg ttattttgtg 540
166 tattcttttg aagtcaaaag ttatttctta catatactct aaaaatatag ccgataccaa 600
167 ttttttccaca catggacttc ctttattcca aaagtcaata aagtgtgacg tcatgatact 660
168 tacgctttaa aacatcgcat gatgatgtca ttagcatcaa tctccaccgt ccaatttatt 720
169 tagttgttga caatatcgac cgtctaagtt ccacaccgac ggctataaga gtttcattat 780
170 aaattttagc aaaataaaat cagcaaataa ttttttcttg actaagctta aacgacgccg 840
171 ttaacatttt cttctggcta acatgaacaa ctctttgaag aaagaagaac gcgtagaaga 900
172 agataacgga aaatctgacg gtaacagagg gaaaccgtcg acggaagttg ttcggacggt 960
173 aacggaggaa gaggtggatg agttttcaa gatattacgg agagtacacg tggcgacacg 1020
174 aacggttgcg aaagttaacg gcggtgttgc tgagggagag ttaccgtcta agaagaggaa 1080
175 acggagtcag aatcttgggt tgagaaactc gttggattgt aacggcgttc gagacggaga 1140
176 attcgatgag attaatcggg tcgggttaca gggtttgggt ttggatctga actgtaaacc 1200
177 ggaaccagac agcgttagtt tatcgttgta gacttgtagt ccttcatgtt tttccccttc 1260
178 ttacaataat caatttttt ttaactacaa tacttttgaa aaaaatggta aaagaagatt 1320
179 attaacatgt tatccaaatt tcagattctt cagttttatt ttatacgtca aaagagaagt 1380
180 tatatatttg caaaactaca agtcaaacaa aagctattta agcgtttgac gttcctaaac 1440
181 aacataaatt ttactaaaat caatgttta aaaaagtgtt gatggtaaag atatcaattg 1500
182 ggcttttgcc tggcccgttt agtaatattg cagagtaggt atgggcctgt ataagggagt 1560
183 ccaaaaaaag agcgggcatt gcgggttggg tgcgtttgga actttggatt gtggattagt 1620
184 catggtttat ctattaatgt ctgcggactt gtggacgacg cgcttgttct tcttcctctg 1680
185 tttacgactt acgaacatat 1700
188 <210> SEQ ID NO: 4
189 <211> LENGTH: 608
190 <212> TYPE: DNA
191 <213> ORGANISM: Solanum tuberosum
193 <220> FEATURE:

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194 <221> NAME/KEY: CDS
195 <222> LOCATION: (124)..(438)
197 <400> SEQUENCE: 4
198 caggtaatac acacagaaaa cattgacata acaqatcgaa tacacattat attatattaa 60
200 tgagagaata aagagaagta attgcactag cagtattgac aattaatcag ctagccggct 120
202 tga atg cta ctt atg gac gga gaa aag aag agg aag aga aca gca atc  168
203     Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile
204       1               5                  10                  15
206 ggc gcc gga gat cgg agt aag gat gag gta gaa gct act gtg aag gag  216
207 Gly Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu
208                  20                  25                  30
210 gag gag ccg ccg tca gag gcg gag gtt gac gag ttc ttc gcg atc tta  264
211 Glu Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu
212              35                  40                  45
214 cgg agg atg cat gtg gcg gtg aaa tat ctc cag aga aat gct cag att  312
215 Arg Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile
216          50                  55                  60
218 cgg ccg gaa aac ctt aac gca tcg ccg gcc ggt gct aac ggt gtc gca  360
219 Arg Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala
220      65                  70                  75
222 gct gga cgg aag aga gaa cgg gga atc gtg aga aaa ggt gat ttg gac  408
223 Ala Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp
224  80                  85                  90                  95
226 ctc aac act ctg ccg gac ggc gga gac taa ttaacgcagt ttaagcatag    458
227 Leu Asn Thr Leu Pro Asp Gly Gly Asp
W--> 228                 100                 105
230 gttaatttaca taaatgcacc cttaattatc gtagatttct aagattgatc tgctgtacag 518
232 attaatttaat taaagccttt ttttatatat atttctccgg taaacggttt gctctttgtg 578
234 attttcttta ataaatttaa tttatttttat                               608
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 104
239 <212> TYPE: PRT
240 <213> ORGANISM: Solanum tuberosum
242 <400> SEQUENCE: 5
243 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile Gly
244  1               5                  10                  15
245 Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu Glu
246             20                  25                  30
247 Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu Arg
248         35                  40                  45
249 Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Arg
250     50                  55                  60
251 Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala Ala
252 65                  70                  75                  80
253 Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp Leu
254                 85                  90                  95
255 Asn Thr Leu Pro Asp Gly Gly Asp
256             100
260 <210> SEQ ID NO: 6
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RAW SEQUENCE LISTING DATE: 01/02/2001
PATENT APPLICATION: US/09/733,685 TIME: 12:08:29

Input Set : A:\PTO.txt
Output Set: N:\CRF3\01022001\I733685.raw

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261 <211> LENGTH: 349
262 <212> TYPE: DNA
263 <213> ORGANISM: Lycopersicon esculentum
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (3)..(233)
269 <400> SEQUENCE: 6
270 ct tcg gag ggt gag gtg gat gaa ttt ttc gca att tta cgg agg atg     47
271    Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met
272      1               5                  10                  15
273 cac atg gcc gta aaa tat ctt cag aga aac gct cag att cag ccg gaa    95
275 His Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu
276                  20                  25                  30
278 aac gtt aac gct cac ggc agc aag tta acc gca tcg ccg gcc ggt gtt   143
279 Asn Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val
280              35                  40                  45
282 aac gga gat gca act gga cag aag aga gaa cgg gga atc gtg aga aaa   191
283 Asn Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly Ile Val Arg Lys
284          50                  55                  60
286 ggt gat ttg gac ctc aac act ttg ccg gac tgc gga gac taa           233
287 Gly Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
288      65                  70                  75
290 cgcagtttaa gcataggtta attacagaaa tgcacctttta attatcgtag attcttaaga 293
292 ttgatctgct gtacaaattta attaaatgaa gcttttttt atatattaaa aaaaaa      349
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 76
297 <212> TYPE: PRT
298 <213> ORGANISM: Lycopersicon esculentum
300 <400> SEQUENCE: 7
301 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met His
302   1               5                  10                  15
303 Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu Asn
304              20                  25                  30
305 Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val Asn
306          35                  40                  45
307 Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly Ile Val Arg Lys Gly
308      50                  55                  60
309 Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
310  65                  70                  75
314 <210> SEQ ID NO: 8
315 <211> LENGTH: 75
316 <212> TYPE: PRT
317 <213> ORGANISM: Glycine max
319 <400> SEQUENCE: 8
320 Met Glu Val Glu Lys Arg Lys Asn Lys Arg Val Met Gly Glu Glu Glu
321   1               5                  10                  15
323 Glu Ser Glu Arg Val Lys Asn Lys Arg Leu Lys Gly Val Glu Glu Glu
324              20                  25                  30
326 Asp Gly Ser Asp Gly Val Pro Thr Glu Glu Glu Val Glu Glu Phe Phe
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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 01/02/2001
PATENT APPLICATION: US/09/733,685 TIME: 12:08:30

Input Set : A:\PTO.txt
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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:537 M:283 W: Missing Blank Line separator, <220> field identifier